Integrative Cancer Research Special Interest Group Teleconference

Pathways SIG Meeting Minutes

Date, Time & Location:	June 1, 2004 1:00 – 2:00 EDT
Attendees:	Cathy Wu – Georgetown Emily Zheung – The Institute for Cancer Prevention Naveen Vinukanda - The Institute for Cancer Prevention Gary Bader – Sloan Vincent Yau – Oregon Health Ajay Jain – UC San Francisco John Rux – Wistar Terry Braun – Holden David Jewell – Dartmouth Simon Lin – Duke Piers Nash – U of C Yajun Yi - Vanderbilt Claire Zhu – BAH Juli Klemm - BAH
Introduction:	**Roll-call, open meeting, review meeting goals** - Review of last meeting - Review Developer/Adopter activities - Identify and define future activities/research areas
Review Discussions:	**Review discussion of last meeting** - The group discussed how pathway data should/could be used. - The link to Pathway resources compendium compiled by Sloan was provided in last months' minutes and will ultimately be make available on the caBIG web site. Currently data-centric, other types of pathway information can be added in the future. - The group discussed emerging pathway standards, PSI and BioPAX. PSI is more relevant to protein-protein interactions and does not support full pathway information. - Developers are encouraged to post information regarding their tools online, so that potential adopters can learn more about the tools they want to adopt. **Review of Mission Statement** - A few feedbacks were incorporated into Gary Bader's' draft mission statement. Juli has formatted it to follow the general mission statement structure. - It was pointed out (by Ajay Jain) that easy data entry by experimental biologists is important for pathway databases. This brought on the discussions on public/private access/versions and needs for tools that allow individual scientists to create pathways from their own data without being restricted by or interfering with exiting curated pathways. **Review of Developer/Adopter activities** - Juli has been contacting centers individually and discussed resources and timelines with each centers as part of the matchmaking process. There were good complementarities among developers and adopters. Verbal agreements on high-

level milestone deliverables.

- Sloan has a number of resources for pathway data and will be working on making these tools compatible with caBIO standards. Oregon Health will adopt the Sloan tools.
- QPACA is under development by UC San Francisco. Oregon Health will also adopt this tool.
- Georgetown will make PIR data available to caBIG and Penn will be the adopter for this project. PIR provides a protein-centric view of pathway information. A great deal of additional data integration work with regard to pathway information has been incorporated recently and will be available in the next release.
- Several centers expressed interest in participating as unfunded Adopters for some of the tools being developed in this SIG. Among these, the Institute for Cancer Prevention would like to adopt Cytoscape of Sloan. Iowa would be interested in making use of any standards/protocols for pathway data analysis. Duke would be interested in evaluating some of the tools.

Future Activities

Presentation of current tools and datasets

- Presentation/demo of tools/datasets by Developers over the next few meetings
  - 15-20 min presentation/demo (PowerPoint or live demo) on each tool, followed by 10-15 min discussions.
  - Should be focused on how the tool will be used.
  - These presentations/demos will be very informal and only within the SIG. The purpose is to facilitate discussions among the group and between developers and adopters.
  - Cathy Wu and Gary Bader will present PIR and BioPAX, respectively, at the next SIG meeting. Juli will follow up on providing resources.

Future research areas

- It may be useful to have a dedicated experimental arm to aid tool development for pathway data analysis. Look into partnering with a wet-lab group generating large data sets that “exercise” an experimental system. The data might include multiple cell lines with multiple perturbations, at multiple time-points, etc. Such a collaboration could be important for testing and validating pathway models/simulations.
- Mining of pathway data from unstructured data sources: This is an active area of development and it may be useful for this group to access the existing approaches. PIR (Georgetown) has an ongoing effort to tag protein names for mining the literature. Wash U’s Function Express extracts gene/protein co-occurrence information from MedLine abstracts and displays network information based on this.
- Full documentation of use cases for pathway information would be important for guiding future discussions of this SIG’s priorities.

Action Items:

Name Responsible	Action Item	Date Due	Notes
Juli Klemm	Distribute meeting minutes	6/4/04	

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[redacted]	Juli Klemm	Work with Webmaster on information organization on the caBIG website	6/18/04	
[redacted]	Cathy Wu, Gary Bader	Present PIR, BioPAX at next month's SIG meeting	7/6/04	
[redacted]	Juli Klemm	Work with Cathy and Gary to get necessary resources for next month's presentations	6/19/04	